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DR. DURKIN: It seems to me that Chris has kind of put his
finger on it here. You folks aren't approaching this from an RFD point
of view, but you are looking at it as a margin of exposure. It seemed
to me that where Chris might be going, and please correct me if I'm
wrong here, is that if the stability, the confidence intervals narrowed
at a higher effect level, that might not be a bad thing to do.

But then you would simply want to say, well, we're not going to accept an MOE of 100, but maybe an MOE of something higher.

And that seems to be a reasonable approach, which is not to say

I think that there is going to be any consensus here that you want to
do anything differently.

I mean, the ED10 is a little disquieting. It's not bringing down the house. You are not going to have folks lined up down on the floor. So it may be reasonable to have an ED10 with an MOE of 100. It could be reasonable to pick an ED50 perhaps and, depending on how the data are, and simply say as a judgmental approach that now we're not happy with an MOE of 100 anymore, but we're going to increase that by some factor.

And I don't know that there is a truly analytical way to get at that. I think that may just involve somebody probably down at that end of the table going out on a long limb.

1	But the gist, I think, of our comments here is that what you
2	have done appears to be reasonable. There are other things that you
3	can think about, but there is nothing really wrong here.
4	DR. KENDALL: I can accept that.
5	DR. BRIMIJOIN: One more comment, then we should turn to
6	some of the other questions.
7	DR. PORTIER: I'm just going to highlight one of the things in
8	my comment, which I have written down. And that is, an objective
9	criteria for choosing a benchmark dose.
10	All I'm asking for is some objective criteria for that. And then
11	we can talk about the risk characterization later. But that's the thing
12	to look for, is why choose 10 or 5 or 1.
13	DR. BRIMIJOIN: The next point that is raised here is a
14	question about the expression of inhalation exposure in the same units
15	as the oral doses.
16	That was something that EPA was told to do by the previous
17	meeting. They have done it.
18	Does everyone agree on that point?
19	THE MEMBERS: Yes.
20	DR. BRIMIJOIN: So that brings us to consideration of the

impact of individual animal data instead of summary information.

1	And Dr	Durkin	hada	comment or	that

DR. DURKIN: Well, I would like to beat my dead horse, if I could, and just get some clarification for my own benefit and the benefit of others who are going to be looking at this method.

When we got together, I guess a couple of years ago, I made a relatively impassion plea for the use of individual animal data. You people would not accept this study if that data weren't there.

I made the point that it is not that hard to get. And it is not that hard to treat. You have been at this for a long time. I honestly think you are going to be at it for a lot longer.

And it seemed quite reasonable to me. I did work that in to the SAP recommendations in the report.

The last time we got together, I thought I heard somebody at EPA essentially say that it can be analytically demonstrated that if we use the mean and some measure of variability associated with that mean, it can be analytically demonstrated that it's just not going to make any difference at all.

And I think I heard a murmur of approval from those statistically knowledgeable around the table here. And again, I will point out that I am not now nor have I ever been a statistician, mathematician or anything else like that. I am uneasy when I read

your response -- and overall, again, I think you have done a great job in responding to our criticisms, but this one you essentially quoted our last report which had a bit of a milk/toast thing about individual animal data are nice, but it probably wouldn't make that much difference. And I think we might have been echoing back what we heard.

I have tried to understand better, read a few things with all sorts of Greek characters that gave me the willies.

We do have a lot of really good stat people here. I just want someone to whack me on the head to tell me that I'm wrong. But this is my understanding. If the measurements from the individual animals are reasonably symmetrically distributed about the model measurement, it is probably not going to make a great deal of difference either in the central estimate of exposure or perhaps even in your assessment of the errors that might be associated with your dose response model.

If on the other hand that is not the case, and for something like acetyl cholinesterase inhibition, I'd rather suspect that especially in the lose dose region, if you have a group of 10 animals, you are probably going to see eight of them that are just honky dory and two that start heading south, that it still could be worth looking at the

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1	individual animal data, at very least to better explicate to people like
2	myself why it is not generally necessary.

3	And at least do it for one or two chemicals to show us that i
4	isn't necessary.

But I really think you have to document it better and in some way qualify it so that if this huge effort that you have undertaken is indeed used, as I suspect it will be used as a model or other similar assessments, there are some guidelines.

And it may well be the case that you can analytically demonstrate that we never have to look at this data. I doubt that's true.

There probably have to be some guidelines given. And I think you should do a fuller job discussing in the document why in this case you have elected not to take that additional step and, again, educate me and perhaps put in at least a single example of here is a case where we use the individual animal data as well as the group data and it just doesn't make a lot of difference.

So I remain very skeptical about the decision. It is about the only criticism I have of what you have done to respond to us, but about this decision to ignore the individual animal data.

I'll get off the soap box now.

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2	DR. SETZER: There are a number of issues surrounding the
3	individual animal data.
4	One of them is the one you have alluded to. And it has to do
5	with sort of the shapes of distributions and the nature of the response.
6	I basically agree with your concerns about that.
7	The other issue, and that was one that people I think we
8	talked about a lot in the last SAP review, had to do with the issue that
9	for the blood measurements, plasma and red blood cell, we had
10	repeated measures on those data sets.
11	And in fact in that case, we can't even do a legitimate analysis
12	of the data without individual animals.
13	Imagine my joy to hear that we have decided to work on brain
14	instead of plasma and red blood cell. We have eliminated that.

DR. DURKIN: It doesn't get you off the hook.

DR. KENDALL: I would welcome a response.

Part of the problem has to do with the relative efforts involved in getting individual animal data for all these chemicals. The data are there, my understanding is, on paper stored away somewhere.

But it changes the relative priorities of various sorts of analyses.

DR. SETZER: I understand that it doesn't get us off the hook.

Turning those into something that we can analyze is doable, but

1	labor intensive and can take time. And I think my understanding is we
2	couldn't get it done before our deadlines.

However, we do have the sort of data sets you are talking
about. We have an example data set. At the moment I can't give you
the details. It is several chemicals and at least more than one study a
least for some of the chemicals

We do have easily -- already extracted the individual animal data. And it is our intention to analyze those data. We just didn't get to it yet.

DR. DURKIN: In terms of some of the problems that you have talked about in optimizing your model, the thing that I have found at least with kinetic studies is your optimization may head south if you use group measurements.

If you do pull in the individual animal studies, a lot of times your models will optimize better.

I'm not making a guaranty here of course. But I'm just trying to encourage the agency to at least think about it.

I know that it is clerical work. And I appreciate that. And you have to QC it. And there is all sorts of troubles.

But it would certainly make me feel better to at least see in the body of your report we don't use individual animal data because it just

1	ain't necessary, or whatever you want to say and to see at least one
2	example to get this guy off our back. It just didn't make a whole lot of
3	difference.

But I do suspect that with cholinesterase it will give you perhaps an insight into what is going on with the animals that could be useful.

7 DR. KENDALL: Dr. Durkin, I think you have made your point.
8 And it's well taken.

9 DR. LOWIT: Can I make one more response? We thought about this a lot.

And Woody is correct. The vast majority of the data we have right this second is in paper in shelves and everything else and have made efforts to make images of the pages and everything else.

We have roughly between 15 and 20 for which we have been able to take TIF images and convert them to electronic data sets. And honestly, I ran out of time.

DR. KENDALL: Thank you.

Dr. Portier?

DR. PORTIER: I'll briefly reiterate a point we made at the last meeting just so it is on the record again this time.

21 And that we would encourage the agency to prospectively think

1	about beginning to collect all of this data electronically for any future
2	studies so that you can do individual animal data analyses.

- Not necessarily retrospectively for this one, but clearly there is some advantage to doing that in the future.
- 5 DR. KENDALL: Good point. Very good.
- Dr. Brimijoin, I know you are going to make it through this first question.
- B DR. BRIMIJOIN: Yes. We're getting close here.
- 9 The last question is about the derivation of oral doses from the 10 actual dietary intake rates.
- 11 Again, that's a cryptic summary of a recommendation from
 12 September. And I take it that the point was measure actual rates.
- Don't just guess what levels are being ingested.
- 14 Is the panel satisfied with the response in the present document?
- 15 THE MEMBERS: Yes.

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- DR. MCCONNELL: I would only add one thing. This is a small point, but it's one that bugs me all the time when I see it, is that exposure and dose are misused quite often in this document.
 - And I think it would for the purists in the crowd it would certainly help that when you talk about dose you are talking about what really is absorbed into the body versus exposure, what we get in

- our food and what we breathe and what we get on our skin.
- 2 And there are two different concepts. For toxicologists, it is
- 3 one of those pet peeve things.
- DR. BRIMIJOIN: Turn this over to the next group?
- 5 DR. KENDALL: Yes, Dr. Conolly?
- 6 DR. CONOLLY: I mentioned this earlier, but I got to read the
- 7 draft cancer guidelines last month. And in the guidelines is a very
- 8 explicit delineation of what they call exposure. I think it is applied
- 9 dose and internal dose.
- And it might be useful, I think, for the agency as a whole to
- harmonize their terminology perhaps in these terms. It is very clearly
- worked out in the cancer guidelines.
- DR. KENDALL: Any further comments from the panel, Dr.
- Portier, for Question 1A?
- DR. PORTIER: I'm going to assume that we have the ability to
- go beyond the list of items here to some of our other recommendations
- that were done and comment on your handling of those other
- 18 recommendations.
- 19 Is that agreeable to you?
- DR. KENDALL: Yes.
- DR. PORTIER: There was one more point which I raised in my

1	questions	but which	I will no	w formally	comment on.

2	And that is the CELs and the use of the CELs in this analysis
3	and the comparison of the CELs to the benchmark dose numbers.

I still believe that this is inappropriate. I still frown upon the agency using NOAELs and LOAELs in any context. I believe the regression based techniques indicate to you when in fact you don't have sufficient information to make a dose response analysis. And to use LOAELs and NOAELs in those situations are just going to be somewhat misleading.

There are a few pathological cases where you might make a good argument for a LOAEL or NOAEL. But I think as a general rule I would prefer regression analysis.

In addition, there are some, I'll call them, throwaway statements, for lack of a better term. In the risk assessment document, they talk about inability to fit some of these data to dose response models, which I find difficult to believe in looking at the data that I was looking at.

So again, I would encourage you to extend the regression techniques across all data sets.

And failure to do that should tell you something about the information you have in hand.

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1	DR. KENDALL: Dr. Reed?
2	DR. REED: I think I was the one who made that comment
3	during the last meeting, that last request about deriving oral doses
4	from actual dietary intake rates.
5	My comment was in the context of when we were looking at
6	where is the beginning of this, 21 days or 28 days or any further. And
7	at the time I understood that the dose was calculated based on an
8	average body weight and consumption rate in a long term study, for
9	example, a two-year study.
10	And it isn't quite sure right now to me if that had been looked at
11	since then or I was under the impression that there was no further
12	analysis since September's meeting about the data sets.
13	Am I correct on that?
14	I mean, did the agency go back and did reanalyze or reenter the
15	dose response based on
16	DR. LOWIT: I believe the document number is III B I'm
17	pretty sure it is 4.
18	There is a section in that document where we did a pilot and
19	somewhat of a pilot using subsets of the studies where each time point

the dietary intake from a window close to the time of the

cholinesterase was measured was used as opposed to the whole study

- 1 average. And that is in that section as a pilot.
- And I assume when they -- this side of the room nods their head that that was okay, that they saw that.
 - DR. REED: That's what I thought. But then it was confusing when there was a statement about half an hour ago saying there is no reanalysis of data. And then I was confused about that.
- 7 So there was. Okay.
 - The other thing is that I probably don't have as strong a feeling against using NOAEL as comparison point when you don't have enough data, but I was also under the impression that with the oral studies there is situations where, because we're using brain cholinesterase inhibition now, that you might not have as many data sets and there is situations where you only have one data set with the oral data.
 - So how does that differ from the inhalation and dermal studies having lack of data? I understand that in certain situations you just can't model it. But I also would like to echo Chris's comment about if it is possible to see how they model.
- I understand that not every case you have the luxury of doing
 that even with one data set.
- DR. KENDALL: Dr. Bull?

DR. BULL: I saved this until last because it's not the most
important thing.

One of the things that I missed as I read through this, and I had to read some parts of it very quickly, I would have liked -- I realize you don't have all the pharmacokinetic mechanistic information you need on all 29 compounds, but as you are going through these processes, as did you when you dealt with the shoulder on the response, it would be useful to kind of check your assumptions against the data that are there.

One of the things I saw no discussion of is -- 4 is more of an example.

The degree of cholinesterase inhibition at any given point in time reaches a steady state based on the rate at which react with the enzyme and the rate which is either regenerated or resynthesized.

And it would have been nice to just kind of touch base with that and say, well, in the rat we know that the enzyme is regenerated with a half line of X, Y or Z.

Some of the -- maybe your shoulder even might relate to the fact that somebody's phosphate esters are going to hydrolyze at different rates than others depending on the structure of the phosphate ester -- and so forth.

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1	If you could find if could kind of spend a little bit of time,
2	not a lot, because you are still going to have to go back, as I think you
3	did to the descriptive data in the end anyway, it would just make those
4	of us that are a little bit more inclined towards mechanism if you bless
5	that part of the effort.

It's just a general comment.

DR. KENDALL: Thank you. For the panel in terms of moving forward here, we will go onto Question 1 B, complete that and take a break.

Then I would like, because we are doing very well, Mr. Lewis here has recommended that we proceed to the next question, which would have been scheduled for tomorrow morning, and to achieve that question today, leaving us to begin in the morning with the assessment of food exposure. That's where I would like to be.

And there is some consideration as recommended to me by Mr.

Dorsey as trying to finish all the panel's deliberation by Thursday evening instead of going into Friday.

I want you thinking about that, EPA.

So we will proceed as deliberately as needed, whatever time is needed, but this is a possibility. And it would, I think, be more efficient in time and resources if that was achieved.

1	Nevertheless, let's go to Question 1 B. And that has been
2	presented to us. And Dr. Heeringa, would you lead off, please, sir?
3	DR. HEERINGA: Let me for the record just read the question,
4	Question 1 B.
5	DR. KENDALL: That will be fine.
6	DR. HEERINGA: Several of these issues were addressed by the
7	application of the nonlinear mixed effect model for combining
8	cholinesterase data.
9	In addition, EPA utilized the profile likelihood method for
10	estimating horizontal asymptotes when they could not be estimated
11	jointly with other parameters. Please comment on the use of these
12	statistical procedures in the dose response assessment of the
13	organophosphate pesticides.
14	I'm going to lead off with a few comments.
15	DR. KENDALL: Yes. Thank you, Dr. Heeringa.
16	DR. HEERINGA: The question of the nonlinear mixed effect
17	model, and that's a long title for a statistical procedure, let's break it
18	down for a moment, it is quite clear that the nonlinear component
19	here, even if we assume normality of the error terms, essentially what
20	we're saying is that the conditional means of these expected responses

are nonlinearly functions of a series of parameters.

1	So that piece is quite obvious.	And I think that has been
2	recognized for a long time.	

But one thing about nonlinear modeling of any sort is that the data must be adapted to estimate the points of inflection in these nonlinear models.

Just my sort of naive exposure to this is that a lot of the dose response studies that we appear to be dealing with appear to be more optimized. In other words, their spacing of dosings in the underlined studies themselves appear to be more optimal for linear estimation such as probe it type dose response regression functions.

And looking through the actual graphs that were presented, which were very, very helpful for me because I'm pretty much a visual person on a lot of statistics, it is quite clear that for a lot of the things that we're dealing with, such as the shape and displacement parameters in the expended model, that a lot of those parameters in the current studies are being estimated in zones of observation where we have very little data.

If you look at it, a lot of times we get data points preceding the inflection points represented either by the parameters in the basic model or the S and D parameters in the expanded model.

And that's not something that the EPA can do anything about.

1	However, I think in encouraging, if we move on to use these models in
2	cumulative risk assessment for organophospates, I think it behooves
3	all of us to begin looking at measurement strategies that are more
4	optimal for estimating these particular models.

I'm going to leave comments about the expanded models for the next question.

The second is really the mixed effect in that here we're talking about mixtures affixed and random effects.

My only comment here is that mixed effect models are very, very useful. And I think that this is an appropriate adaptation of mixed effect models.

Now, we have to remember what we -- when we include random effects in models, you essentially -- random effects are included to reflect effects of things that pretty much are random in the observation process, like the animals themselves, their responsiveness, whether you get a particular batch of rats that has a particular disposition to cholinesterase inhibition.

We expect that to vary about some mean for the standard series of rats that are being used or other animals that are being used, the particular preparations, which might be errors at the local level, but they may vary about calibration standards or other forms of

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One of the things that we're including in these models as a random effect are essentially the data sets within the studies.

And I asked the question this morning about what distinguishes those. And the point comes up that duration may distinguish one data set from another.

And I had asked the question if we're treating data sets as random effects, we're really treating duration as a random effect. Is duration a random effect or a fixed effect in modeling cholinesterase inhibition.

These are sort of rhetorical questions which I ask myself. And they are not criticisms. But you need the minimum of two observations to estimate a variance.

And when we get into these random effects, one of the principles here, and without looking at power E calculations, but we need to have a significant number of observations on the random effect itself.

And if that is a study, we need to have I believe more than two studies to be pretending they are random effects. Otherwise, we could say we have effective a particular individual or a particular teacher.

But if it is Mr. Smith and Ms. Jones and those are the only two

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- observations we have, we really have fixed effect to Mr. Smith and Ms.
- 2 Jones. And we're averaging that.

So we have to be a little bit careful in using the mixed effect model here when we have a very few observations on a particular random effect that we're trying to model.

One other question I had related to random effects too, and I should have asked it earlier, and that is is there any way that we can reflect the degrees of freedom. And that is the statistical information in these data set means and standard deviations.

In other words, the quantities going into these models are actually estimates of means which are based on varying numbers of individual observations on individual animal subjects.

And there is information there that in terms of degrees of freedom that is not being reflected unless it's somehow being built into as some sort of weighting for the actual variance of the mean that has been estimated.

Finally, on the use of the profile likelihood, the whole issue of data density arises here as well. We all know full likelihood is really a function of the distribution that we assume. Here it is normal with a conditional mean and defined by the exponential functions and the amount of the individual data.

Look at the graphics that were presented in this report. And
they are excellent. I understand some of it has been redone, but I
wouldn't expect these conclusions to be completely overturned. When
there is data, the profile likelihood is very well defined. Obviously,
decisions to use a profile likelihood method to fix values of some of
these parameters that can't be separately estimated I think it makes
sense.

Other cases, though, and it generally happens when other parts of the modeling break down, the profile likelihoods often wind up being sort of ill-defined or somehow narrowed to a fairly wide plateau on the likelihood function.

For example, I noticed very rarely, though, if the model fits well to the data, and just by physical inspection, if the model fits well to the data, these profile likelihoods are fairly well-defined.

If they're needed to fix values of these asymptotes for lowest threshold or lower level of effect, I think that it is probably an appropriate use.

Some things -- I only noted one case. And that was dichlorovos where in the profile likelihood, and again, this may change with the analysis that has been done subsequently, you get a saddle likelihood. The model fits well, but the profile likelihood has this sort of saddle

1	shape

2	So you don't know whether to go to Hill A or Hill B. You	are
3	sort of stuck in the saddle in between.	

Profile likelihoods for the expanded model when I looked at those, they are -- when -- are informative at all, really. I felt they are primarily limited to knowing that the displacement is a very small number. And with a fairly wide range, don't do much to narrow the region of the optimum on the shape function of the curve.

So essentially, it informs us a little bit about how large that displacement might be in the model, but, again, leaves us pretty much wide open with the data to choose an optimum S.

The benzylthide (ph) example which we saw in the screen here and which I noted in my own notes was probably the exception. That had the nicest sort of by more to likely or by very -- profile likelihood for the expanded model.

In general, I would say that I think that as a general model, the nonlinear mixed effect model is appropriate.

And in cases where we have a good number of studies and a rich base of data that spans a wide range of doses, it appears to work well and is clearly the preferred model.

I think like everything else in statistics when we begin to run

- out of data, all of this begins to become a little more questionable.
- 2 And I really don't have any alternatives for those situations
- 3 where we're in the situation of sparse data, except to get more data,
- and that doesn't help you right now.
- 5 DR. KENDALL: Thank you, Dr. Heeringa.
- 6 Dr. Portier, Dr. MacDonald?
- 7 Dr. Portier will go first.
- 8 DR. PORTIER: I will read the points I put down up to this
- 9 point.
- 10 I think the mixed effect model corrected for many of the
- problems we highlighted in the previous review. So I think a lot of
- things have been taken care of that we talked about.
- In terms of the comment concerning the profile likelihood or
- the question concerning the profile likelihood, my intuition in looking
- at this is that if the optimization, if the algorithm used for
- optimization dealt with boundary value problems, you would probably
- skip that profile likelihood step.
- It seems to me in the way you are doing the profile likelihood
- visually and saying, well, this one is going to converge, but that one
- doesn't, the failure to converge is at the boundary value situations.
- 21 And so it's the log transforms, the inability to go to actual zero

is the thing that may be driving the lack of convergence more so than
 an actual failure to find an optimum.

And I think you should -- one suggestion is to look at that. I don't think it will have any impact. Because the choices you are making in the cases where you are getting stuck to the boundary is exactly the choice in algorithm that dealt with the boundary value problem we deal with.

I will reiterate that clarity of the model and methods would be greatly appreciated. Again, showing a model in mathematical form that talks about the variance construction and the fixed and random effects that go on would be useful.

One point that comes to mind in hearing Dr. Heeringa's comments just now is that in the decision tree where you were evaluating how to move through the various models, it is a good question to ask why go to a single B value with a random effect as compared to a fixed sex effect B value as the third voice.

And the fact that you never choose the third choice may be simply because the third choice and the second choice are effectively equally parameterized.

And you would pick up the sort of almost the same likelihood in the two separate cases.

And finally, one concern for me is the actual expanded model
itself. In essence, you have gone from the basic model to the
expanded model, and you have jumped in two parameters in doing it.

One parameter deals with sort of a shape issue and the other parameter deals with sort of a point of discontinuity breakpoint off the zero Y axis response point.

It might be interesting in thinking about how to move forward with this to separate those two issues out and ask yourself do I really need a shape parameter or do I really need a point of discontinuity on the zero response point, and choose one or the other rather than having to choose both in the analysis.

Because I am concerned about them collapsing in degrees of freedom as they both get towards zero or infinity depending on the parameter you are looking at in the expanded model.

DR. KENDALL: Any questions from EPA? Dr. Setzer?

DR. SETZER: I would like to respond. If I can remember the points, I want to respond to a couple of those points.

As to the issue of basically -- the first part was sort of the issue what is going on. How come we can't always estimate this horizontal asymptote.

And Dr. Portier has said that it has something to do with -- has

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to do with not being able to get to zero for the parameter on the right scale.

One of the things I have done, since December, and it's not anything you have seen or I didn't talk about it today because it is complicated to describe, and I'm not sure how -- if it was worth spending a lot of time on, but I'll bring it up.

There is an approach to analyzing parameter redundancy in nonlinear models, which essentially looks at the degree to which over the -- either for an experimental design or sort of over a range of the independent variables, the degree to which parameters and the model sort of -- multiple sets of values for the sets of parameters can give you essentially the same model shape.

And I applied that to the specific designs we have in this study.

What happens is that the models where we have to fix a piece of B or we have to affix B are exactly those chemicals where the degree of association between the benchmark dose estimate and the piece of B are highest.

So basically what happens is we could -- is that if you adjust piece of B a little bit, you can also adjust the benchmark dose estimate a little bit to give you essentially the model shape.

I don't think that is a function of the transformation used. I

1	think that's actually a function of the designs that we have to work
2	with.

- I have forgotten my second point. So I'll let it go.
- 4 DR. KENDALL: Dr. Portier?
 - DR. PORTIER: I do agree that there are going to be cases where the estimate of P of B is going to be so unstable that anything in a broad range is going to work and you are going to get extremely flat likelihoods. That should be reflected in the variance, not necessarily in the convergence of the algorithm plus or minus error.
 - So the only problems I have ever seen in convergence of algorithms for optimization are: One, I set my criteria for convergence to be too tight.
 - Two, I have got multiple modes, I've got multiple humps. And one time I get this one, another time I get that one.
 - And the third time is I have got nonidentifiability, and I just don't know it. I have parameters that are so correlated with each other that finding one value adjust the other value, and there is just an infinite number of solutions, which is sort of what you are talking about in the case of P B.
 - But the worst one I have ever found, the one that always hits me is when I don't deal with the boundary value problem the way I should

1	deal with the boundary value problem. And I try to log transfer my
2	values and it keeps trying to go to negative infinity, and it just can't.

3	It can't ever converge because it just keeps chopping away litt	tlε
4	pieces and parts.	

And algorithms that specifically project you on to the boundary and then send you along that boundary can converge quicker in those situations than things that try to log transform you along that way.

I think it is worthwhile in future derivations of your code to look for an optimization algorithm like a David and Fletcher Powell or a gradient -- B F G S modified David and Fletcher Powell to deal with the boundary conditions.

DR. KENDALL: Dr. Rhomberg?

DR. RHOMBERG: I hesitate to say this because we have been already raising the question about how biologically interpretable the shoulder equation is.

But if you send that all the way to zero by allowing yourself to do that, by dealing with the boundary value like Dr. Portier is suggesting, that is also, I think, equivalent to making K M equal to zero.

And if that kind of a biological explanation is the cause for the statistical problem which you have here, that causes all sorts of other

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- If there really is a detoxification step that gets saturated at such low values that K M is not detectably different from zero, that's going to affect the pharmacokinetics of other O Ps that are co-occurring.
- And when they are not tested one by one, that's already an issue that will come up later, I think.
 - And so I guess I would hesitate to say this is just an estimation problem and we should let it go to zero if it wants to.
 - We should worry something about the biological basis of this, even if we're not trying to turn it into a pharmacokinetic model to make sure that we're not doing something statistically that would cause it violence to the biological hypothesis of the reason for the phenomenon in the first place.
- DR. KENDALL: Thank you.
- Dr. Conolly, Dr. MacDonald?
- DR. CONOLLY: I think Lorenz just made a good point for why
 you want to call it an empirical model. I think as long as you call it an
 empirical model, then you don't have to worry about the interpretation
 of K M too much.
- Otherwise, I agree with Lorenz.
- DR. KENDALL: Dr. MacDonald?

reasonableness of the model.

1	DR. MACDONALD: I agree pretty much with everything that
2	has been said so far. So I'm not going to repeat that.
3	But I think in talking with Dr. Setzer and listening to his
4	presentations, it is really a work in progress. You have made a lot of
5	changes since the material we got as a handout was prepared.
6	So I would assume that this isn't really the final version and
7	that you are going to continue to refine it. I think you will probably
8	have more success in fitting when you have tried a few more things.
9	Certainly, one advantage of working in R is that not only do you
10	have access to the source code, but you know who wrote it, and you
11	have access to the developers.
12	And generally speaking, they are very helpful if you want to
13	modify or improve it. So that's another very useful route to go.
14	This issue of whether to iterate on logs or on the original
15	parameters is something I have been dealing with in the last few
16	months. And what Dr. Portier and Dr. Setzer have said I agree with.
17	I don't have an answer yet, but it is just the sort of situation
18	where with experience you eventually do better.
19	I think, though, that we shouldn't get too hung up on the
20	inability to estimate all the parameters or even on the biological

we're tweaking.

1	I think much of this is a red herring. Because really, all we're
2	trying to get out of this is a BMD 10. In most cases, you don't need to
3	have accurate estimates of all the parameters to get a good BMD 10
4	out of it. The stability of that estimate is really what we need to be
5	looking at.
6	But it is a very elaborate mechanism that has been set up to get
7	one number when you have to get so many other numbers in the
8	process.
9	Though, certainly, the idea of using the mix model and
10	combining studies, that introduces the extra variances. But I think
11	they are of interest in their own right for the sorts of people that like
12	thinking about variability.
13	DR. KENDALL: Thank you. Any further comments to this
14	question?
15	Dr. Portier?
16	DR. PORTIER: I want to make sure a comment I made is not
17	lost. I think all of my comments will have minor impact on what is
18	actually done here.
19	I think the basic point for comment 1 B is that much of what we
20	wanted, much of what we asked for, has been done. And I think now

deliberation.

1	DR. KENDALL: Well said.
2	I guess the long story made short is you have done really well
3	since the last review and congratulations. I'm going to close this
4	session. We'll take a break. 15 minutes.
5	Dr. Perfetti, I would like to begin the assessment, the next
6	question, the hazard and dose response analysis.
7	Okay?
8	If you have any comments you want to make as we begin that.
9	DR. PERFETTI: Question 2?
10	DR. KENDALL: Yes.
11	Think about that after the break. That's what we will begin
12	with. So a 15 minute break. Thank you.
13	(Thereupon, a brief recess was taken.)
14	DR. KENDALL: We'll reconvene the SAP meeting to now the
15	session to deal with hazard and dose response analysis.
16	Dr. Perfetti has relayed to us he has no opening comments he
17	needs to make in order to encourage the panel to move forward.
18	I would like to ask EPA to put the Question 2 on the screen,
19	which they have done.
20	If they could read the question for us and then we will begin our

DR. LOWIT: An exponential model was utilized by the agency
in the July 2001 Preliminary Hazard and Dose Response Assessment of
the Organophosphate Pesticides. Based on the equation used in the
July document, cholinesterase activity decreases linearly in the low
dose region of the dose response curve.

Stakeholders present at the technical briefing in August of last year and also a few members of the Science Advisory Panel from the September meeting suggested that a flat low dose region may be a more appropriate modeling approach. In response to this issue, EPA has further investigated the shape of the low dose region of the dose response curve.

Two versions of the exponential model were used in the December hazard and dose response assessment. One version called the basic model describes a linear low dose region and is similar to the approach used in the July document. All 29 OPs were fit to the basic model. A second version called the expanded model incorporates two additional variables, shape and displacement, which describe a low dose flat region.

The female brain cholinesterase data supported a flat low dose region for eight OPs, which has now been revised to, I think it is, 17 -- 17 once the errors in the code were fixed.

1	We would like you to comment on the mathematical derivation
2	of the expanded model in addition to the use of the profile likelihood
3	method for estimating the shape and displacement parameters when
4	they could not be estimated jointly with the other parameters.
5	DR. KENDALL: Thank you. Dr. MacDonald, you are to lead
6	off.
7	DR. MACDONALD: I feel that this has already been quite
8	fairly discussed in previous questions. I don't have a lot to add. In
9	fact, I used up my best ideas already.
10	So I'll just comment that I think that this model is very elegant
11	in the fact that it has a very simple biological basis. We don't have the
12	data to support anything more elaborate.
13	And I think with a little bit more experience we might have more
14	luck in fitting it over a wide year class of data sets.
15	DR. KENDALL: Thank you, Dr. MacDonald.
16	Dr. Harry?
17	DR. HARRY: As we were already trying to poll whether we
18	thought this had been covered or not, I think a number of us thought
19	that it had.
20	The only questions I like the biology that was behind trying

to come up with this. It seemed well thought out. And that was a very

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The question that I had raised was based upon that, and I tried
to raise that earlier in the quality of the assays for comparison. And I
talked with Dr. Brimijoin over the break, and we were sort of talking
two different things when we were talking. And I feel very
comfortable with the assays that you guys are using for the enzyme
assays, that they are pretty comparable for potency chemical A to
chemical B on the assays.

My only hesitancy would be to cross that over to a lot of other types of assays that may not be as equivalent between them.

But as far as the approach, like was mentioned, I think most of your statisticians around the table have made their comments. I can only come at it in a biology. And I was impressed with the thought process that went behind trying to pull that out and getting that low dose expression of what may be happening with that shoulder effect.

DR. KENDALL: Thank you. Dr. Rhomberg?

DR. RHOMBERG: I think also that most of my comments have actually come up somewhere along the line already.

I guess I would like to just spend a second, though, reiterating this notion that even though we're being empirical here, and I think you made a very clear point of the fact that this is an empirical factor

that is not intended to be a physiologically based pharmacokinetic
model, it is only being inspired by some possible biological
explanation, that it is worthwhile thinking what biological
phenomenon could account for it in principle.

And do we know enough about them from other sources of data, not from the shape of the dose response curve, to say whether that's plausible or not.

And beyond whether it is plausible or not, if you invoke those phenomena, what would those phenomena, then, say about other situations. And I touched on this briefly before.

What this is basically saying is that the main pharmacokinetic thing of concern here is other kinds of esterases in the liver that are able to metabolize these things away before they really get a chance to do their dirty work on acetyl cholinesterase inhibition.

How many of them are there? This is something I don't know very well. How specific they may be.

But the possibility arises that if that is really the case that that is going on, then low doses to some of these ones that have shoulders big enough to sort of be in the shoulder region there, or getting to the end of their shoulder region are saturating some of these enzymes.

And it will affect the way other compounds go in their relative

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What affect will that have on the compared potencies that compounds have at the low doses where they are actually being experienced compared to the BMD 10. And I think it is just worthwhile thinking through those issues.

Not that you can do anything about them with dose response data. I agree, you can't. But trying to bring some of these other things in just sort of as a reality check I think is important.

It occurs to me that if this really is a pharmacokinetic phenomenon, to a large degree it should probably also apply to the same compounds for the RBC data. And not quite in the same way, since, I suppose, there is not really a first past exactly in the same way for the RBC, since it gets to the blood first no matter where once it gets into the blood.

But nonetheless, this isn't really strictly a first past phenomenon anyway. I think it really is just a matter of saturation of metabolic clearance. That should apply to the same compounds for the RBCs.

And the question then is in looking at the RBC dose response data, do you get the same kinds of things for the same compounds.

It would be interesting if you did. And if it was completely different, it would make you wonder a little bit about the biological

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I think that the issue of actually estimating the two parameters for this, we have gone on about a lot, and I think I have made my point there as well, which is that for the purpose of just using this as an empirical factor for the dose response curves, the difficulty in the S and D issue doesn't really make an awful lot of difference.

The reason that it is difficult is because it doesn't make a lot of difference. So it is not really something to be worried about too much.

On the other hand, when the biological consequences of that, if any, come into play, if they do, then those issues do become important, the relative importance of S and D, because that influences the shape at the low dose part of the curve, which is where small doses of the OPs would be and where their relative potencies would actually be coming into play. And that would be important to work through.

But I would encourage working those things through not with the S and D that you fit by this empirical thing, but actually trying to go to real pharmacokinetics to do it at that point.

That's all.

DR. KENDALL: Anything to add, Dr. Conolly?

DR. CONOLLY: No.

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end.

1	DR. KENDALL: Dr. Durkin?
2	DR. DURKIN: Again, a lot of what has been said covers this
3	topic.
4	I simply wanted to say that when I first looked at what you had
5	done, the term that crept to mind, not to get too technical, is I thought
6	it was cute as a button.
7	I did not have the chance to pop this into mathematic. I'm
8	assuming that the arithmetic is more or less correct.
9	And I thought you did a very nice job of making that transition
10	from we have an empirical model here but we tried to at least base it
11	conceptually on something biological.
12	I too agree that the best thing to do is a formal PB PK PD
13	analysis. I'm not really convinced we have the data yet to do that.
14	If you were to go away and work on this for another decade and
15	get the experimentalists involved in giving you the kind of information
16	that you need, you probably can do it at some point.
17	I don't know that you can do it now. I have poked around a bit
18	in the literature. I think there is stuff out there. I saw on a break
19	Vicki was kind enough to at least give me a peak at some work that

you guys are doing that I think is worth pursuing on the PB PK PD

But I think you did just a really nice job of admitting, frankly,
that we can't do a biologically based model. But you have come up
with an approach that I think is just fascinating to at least give us a
taste of a biological basis for the dose response model.

So I'm extremely happy with what I saw.

DR. KENDALL: Dr. Bull?

Thank you, Dr. Durkin.

DR. BULL: This is just to add. One of the things I noted is we selected female brain cholinesterase activity inhibition because it was empirically more sensitive.

Just to add a little bit I think to what Lorenz was saying, it would be real nice to know how that played out in the male brain cholinesterase. Because often, metabolic differences are accounting for that and you might get some consistency or explanations for the difference between the sensitivity in the male and female and be very intellectually satisfying to say, yes, we picked the right one.

Otherwise, you are sitting there without really knowing a basis of the difference in sensitivity. Up to this point in time, I looked at your graph. I was pretty well convinced that the females are more sensitive. But that doesn't mean that number 30 is.

So you kind of need to know what the basis of those things are

- as you take it down to the next group of registered pesticides.
- 2 So it would be nice to know what the basis of that is.
- 3 DR. KENDALL: Any further comments? Dr. Portier?
- DR. PORTIER: I was going over my notes from all the public commenters to make sure that your promise that additional questions that they wanted to ask the panel would be addressed by the panel, but I don't see any other than the BMD 10 to BMD 01 question that pertains to dose response.
 - The rest pertain mostly to exposure. So we'll deal with them tomorrow.

I did have one comment, something for you to look at and think about. I do not have an answer for. In looking at the expanded model versus the basic model, you have eight cases where the expanded model is significantly improved over the basic model, as I understand what is presented to me in the tables.

And there may be a number of reasons why that occurs. But let's talk about what it means. And I don't think you talked about what it means. I think you talked -- you enumerated it for me, you pointed out that there were these cases. But what does this mean in terms of what is a general shape of a dose response curve for this type of effect and this type of population.

Is there something that can be drawn out from that? For
example, you did 29 analyses. And so had you seen only one in 29
analyses that was statistically significant, one might conclude that this
is not major nonlinearity in the dose response for this type of pattern.

The fact that you see eight significant out of 29, and it's actually less than that because some of them don't fit, does that tell us something about the presence or absence of flat regions in the dose response curve as a general rule in this data?

Had we addressed the data in the opposite way instead of testing the hypothesis in the sense that we reject the higher order nonlinear model in favor of the linear model, but going the other way would we be looking at a different picture.

So I think as an agency you need to look at this and decide would it be more appropriate even though overparameterized to use the nonlinear or the more flexible model as a general rule in evaluating these data simply because you see it eight times significantly better across these data sets.

I don't have an answer, but I would love to see some discussion of that in looking at what you are doing in here.

DR. KENDALL: Any further comments? Then that will conclude our Session 1, hazard and dose response analysis.

т	margaret, we are prepared to move forward to session 2,
2	assessment of food exposure, should you want to.
3	DR. STASIKOWSKI: We would prefer to wait until tomorrow
4	morning to start the discussion.
5	DR. KENDALL: Could you be prepared tomorrow to be ready
6	to proceed through Section 2, assessment of food exposure and the
7	assessment of drinking water exposure?
8	DR. STASIKOWSKI: Yes.
9	DR. KENDALL: I think we will probably be able to get at least
10	through those two sessions, at least, if that would be possible.
11	DR. STASIKOWSKI: Yes. And if we're ready to start
12	residential, we'll be ready for that as well.
13	DR. KENDALL: Outstanding.
14	I ask the panel to get a good night's sleep. We may go further
15	than we think tomorrow.
16	Nevertheless, this has been an excellent day. Really incredible.
17	The word's incredible, the progress you have made. And quite
18	seriously, there have been no real serious criticisms outside of the fine
19	tuning and looking at procedure that can be best clarified and justified
20	This will conclude our session today. And we will reconvene at
21	8:30 in the morning.

1	And I would like to ask if our designated federal official for the
2	meeting, who I have enjoyed working with, would like to have any
3	comments for the panel or other administrative issues.
4	MR. LEWIS: Thank you, Dr. Kendall, for moving us along
5	today and keeping us, if you will, ahead of schedule in allowing for a
6	good deliberation by the panel and for comments from a couple
7	commenters and allowing the presenters to move along at a good pace
8	If I could ask all the panel members to reconvene in our
9	breakroom at 4:15, I just want to discuss with you about any
10	assistance you may need for compiling your comments and in terms of
11	drafting your responses as part of the discussion today. I would
12	appreciate it.
13	DR. KENDALL: This will close our session. Thank you.
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16	[Whereupon, at 4 p.m., the
17	meeting concluded.]
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